

EXPLOITING NATURAL VARIATION IN A TREE SPECIES TO COMBAT AN INVASIVE FOREST PATHOGEN

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Invasive microbes, causing diseases such as sudden oak death negatively affect ecosystems and economies around the world. The deployment of resistant genotypes for combating introduced diseases typically relies on breeding programs that can take decades to complete. To demonstrate how this process can be accelerated, we employed a genome-wide association mapping of ca. 1,000 re-sequenced *Populus trichocarpa* trees individually challenged with *Sphaerulina musiva*, an invasive fungal pathogen. Among significant associations, three resistance loci were identified and predicted to encode a putative membrane-bound L-type receptor-like kinase and two receptor-like proteins. A susceptibility-associated locus was predicted to encode a putative G-type D-mannose-binding receptor-like kinase. Multiple lines of evidence including allele analysis, transcriptomics, binding assays, and overexpression support the function of these genes in mediating this interaction. Herein we demonstrated how the power of population-wide re-sequencing of undomesticated, non-model plant species could accelerate the mitigation of emerging diseases in native ecosystems.

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